- Total



1/11

cons.aa	G G G V	•	A K	E	
hTGFBR-11	LDTLVGKGRFAEVYK	AXLKONTSEOFET	/AVKI FPYD!	YASWIDRIDI FS	DINLAHENILOF
mActR-IIB	LLEIKARGREGCVWK				_
mActR-II	LLEVKARGREGCVWX				
daf-1	LTURVGSGREGNVSR				
subdomains			11	III	īv
	•	•	••	***	• •
					:•
hTGFBR-II	LTAEERRTELGKQYW	LITAFHAKONLOE	(LTRHVISW	DLRNVGSSLAR	LSHLHSDHTP-C
mActR-IIB	IAAEKRGSNLEVELA				
mActR-II	IGAERRGTSVDVDLA			•	
daf-1	IGSDRVDTGFVTEL				
subdomains		V			7I+A
		• .		•	
cons.aa	DLK	N	DFG		
hTGFBR-II	-GRPR-PIVHRDLKS	SHILVENDLTCCL	DFGLSLRL.	GPYSSVDDL	unsgovgtarymap
mActR·IIB	GEGHKPSIAHRDFKS	KNVLLKSDLTAVL	DFGLAVRF	· · EPGKPPGD · ·	THOOVGTRRYMAP
mACTR-II	-DGHKPAISHRDIKS	KNVLLKNNLTACIA	DFGLALKF	EAGKSAGD	THCOVCTRRYMAP
daf-1	· ESNKPAMAHRDIKS	COLLACTIONS	DIGLSLSKI	PEDAASDIIAN -	ENYXCGTVRYLAP
subdomains	VI-B		VII		VIII

Fig. 1

2/11

a.a C C E G N M C 5' GCGGATCCTGTTGTGAAGGNAATATGTG 3' Fig. 2A BAMHI C C G C

a.a V A V K I F

5' GCGGATCCGTCGCAGTCAAAATTTT 3' Fig. 2B

BamHI G C G G C

T T T A

a.a R D I K S K N

5' GCGGATCCGCGATATTAAAAGCAA 3' Fig. 2C

BAMHI A C C GTCT

G A

a.a E P A M Y

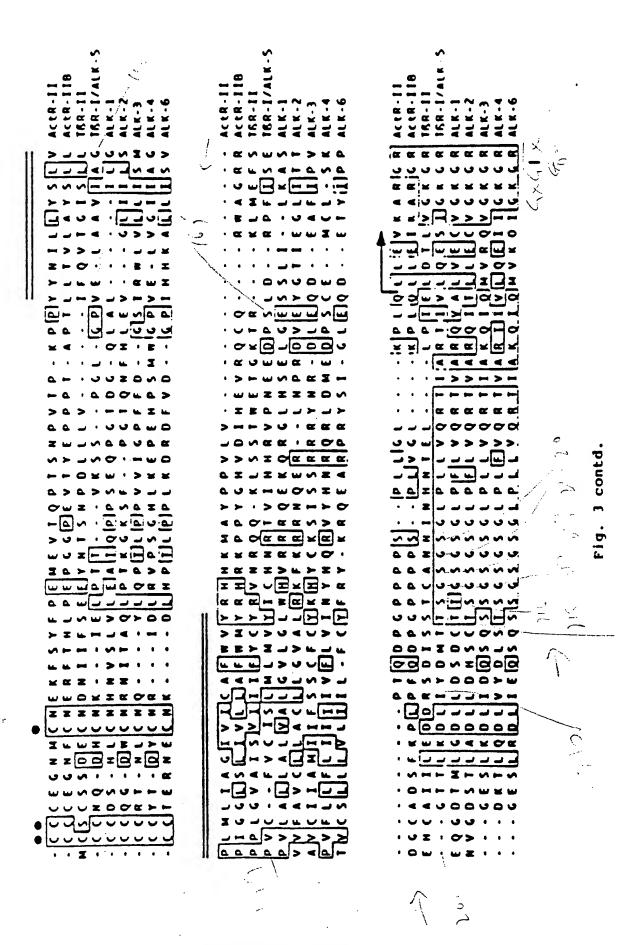
5' CGGAATTCTGGTGCCATATA Fig. 2D

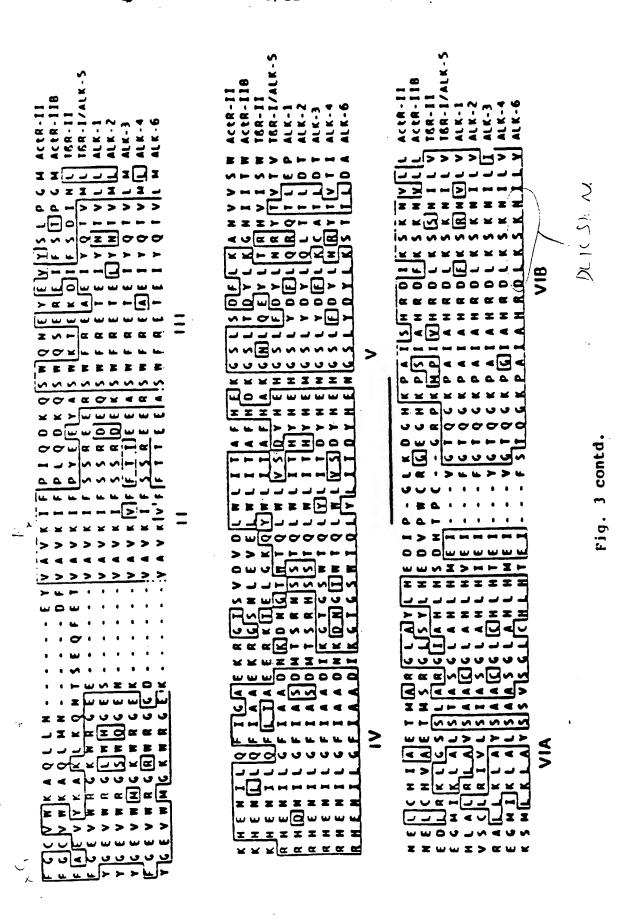
ECORI G G

A A

188-1/ALK-S <u>ے من نہ من من</u> ««40<0×00 ------ 00 - 2 - 2 x 0 - x<u>000000</u> J 0 • Œ FF ECOCOCI * **KKOL->><** ر > - wooooo I ۵ R ~ ~ @ - ~ 0 0 0 0 I

ig.3

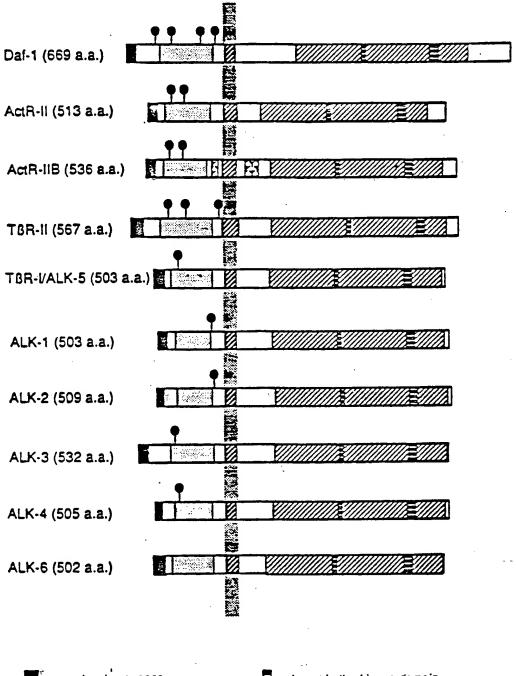




~ D W W W W 00000 ---100 I I mode x oco m > m区の<u>x x x x</u> 000 4447 > = 🖃 101>04+0 >=>>> 0EV-18 8 8 -<u>----</u> · UZZUUU z z z <u>v o o</u> o D o 0 0 0 E & & F O F WIZZZZZ REEN LEBE > = L & & & & E & · _____ 00000000 NANDOZZOZ FROCOCEOR FRECOCE R (프로필마됨 ~ REQUEST V QQKEKE & ししソンドドリート OOUNEENSO

Fig. 3 contd.

Fig. 3 contd.



signal sequence insert in the kinase domain

cysteine-rich region potential N-glycosylation site

transmembrane domain alternatively spliced region

serine/threonine kinase domain

Fig. 4

ActR-11B/CR ACTR-II/CR ALK-1/CR ALK-2/CR ALK-3/CR ALK-4/CR ALK-5/CR ALK-4/CR Ma jor Ity G ۵ BEDNESSE H6>H03< U N < > > × × × 0 _ ۵ ی OOK > ZUUNX 1 100 w #421120 < 1000 1 1 m0 1110000 ŧ 002001101 000000000 Ç MU MEY FFE ш TRPTE - FVNHY
SPRAOLERTIE
SSRTGSVTTTT
KKDPPE - VYFF
KKDPHALLERY
TEENPO - VYFF
KKDPHALLERY
TEENPO - VYFF
KKDPHALLERY
TKRPFFFM OFFH<< - H = H + H = H | 2112251 G ۵ MZIIKK+ ZH>LXXH S ZZZGGV ← × U111 X Q U Z ۵ RHOOGXFEZ ທ OND SE WANT · PONOGe ≻ × G 3 F X W Z L × 10000000 w 10022 7 0 7 EDGE : IGA 10000 1 1 K F 101481140 1 1 교육 2 교육 2 エ I B B D F O F F THE BEACH COLUMN CANDON ۵ U 10001100 U G MOT> XXXMI ∢EE ≻EU ∪ 1 1 1 3 4 X X w KEOTY 000000000

19.

10/11

	ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TBR-II	daf-1	
	79	60	61	63	40	40	37	39	ALK-1
_		63	64	65	41	39	37	39	ALK-2
			63	65	41	38	37	39	ALK-3
				90	41	40	39	42	ALK-4
				्र सुर्देश्य	42	40	41	43	ALK-5
				•		78	48	35	ActR-II
						-	47	32	ActR-IIB
								34	TBR-II

Fig. 6

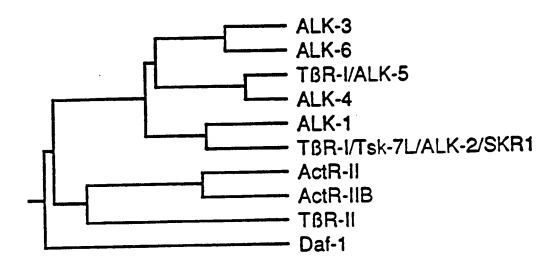


Fig. 7